

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/587,841
Source: IFWP
Date Processed by STIC: 08/08/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 08/08/2006

PATENT APPLICATION: US/10/587,841

TIME: 09:27:23

Input Set : A:\082368-008600US.txt

Output Set: N:\CRF4\08082006\J587841.raw

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4 <110> APPLICANT: Nakagawa, Tomoko
5     Kurei, Syunsuke
6     Toji, Shingo
7     Okabe, Ayako
8     Kuhara, Motoki
9     Kishi, Yoshiro
10    Yahara, Ichiro
12 <120> TITLE OF INVENTION: METHODS FOR ISOLATING MONOCYTES
15 <130> FILE REFERENCE: 082368-008600US
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/587,841
C--> 17 <141> CURRENT FILING DATE: 2006-07-26
17 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/000923
18 <151> PRIOR FILING DATE: 2005-01-25
20 <150> PRIOR APPLICATION NUMBER: JP 2004-018747
21 <151> PRIOR FILING DATE: 2004-01-27
23 <160> NUMBER OF SEQ ID NOS: 6
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 669
29 <212> TYPE: DNA
30 <213> ORGANISM: Mus musculus
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(669)
35 <223> OTHER INFORMATION:
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39 Met Pro Trp Thr Ile Leu Leu Phe Ala Ser Gly Ser Leu Ala Ile Pro
40 1          5          10          15
42 gca cca tcc atc tcc ttg gtg ccc ccc tac cca agc agc cac gag gac      96
43 Ala Pro Ser Ile Ser Leu Val Pro Pro Tyr Pro Ser Ser His Glu Asp
44          20          25          30
46 ccc atc tac atc tcg tgc aca gcc cca ggg gac atc cta ggg gcc aat      144
47 Pro Ile Tyr Ile Ser Cys Thr Ala Pro Gly Asp Ile Leu Gly Ala Asn
48          35          40          45
50 ttt acc ctg ttc cga ggg gga gag gtg gtc cag cta cta cag gcc ccc      192
51 Phe Thr Leu Phe Arg Gly Gly Glu Val Val Gln Leu Leu Gln Ala Pro
52          50          55          60
54 tca gat cgg cct gat gta aca ttc aat gtg act ggt ggt ggc agt ggt      240
55 Ser Asp Arg Pro Asp Val Thr Phe Asn Val Thr Gly Gly Gly Ser Gly
56 65          70          75          80
58 ggt ggc ggt gag gct gct ggg ggg aac ttc tgc tgt caa tat ggt gtg      288
59 Gly Gly Gly Glu Ala Ala Gly Gly Asn Phe Cys Cys Gln Tyr Gly Val

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60          85          90          95
62 atg ggt gag cac agt cag ccc cag ctg tgc gac ttc agc cag cag gtg 336
63 Met Gly Glu His Ser Gln Pro Gln Leu Ser Asp Phe Ser Gln Gln Val
64          100          105          110
66 cag gtc tcc ttc cca gtc ccc acc tgg atc ttg gca ctc tcc ctg agc 384
67 Gln Val Ser Phe Pro Val Pro Thr Trp Ile Leu Ala Leu Ser Leu Ser
68          115          120          125
70 ctg gct gga gct gtg ctg ttc tca ggg ctg gtg gcc atc aca gtg ctg 432
71 Leu Ala Gly Ala Val Leu Phe Ser Gly Leu Val Ala Ile Thr Val Leu
72          130          135          140
74 gtg aga aaa gct aaa gcc aaa aac tta cag aag cag aga gag cgt gaa 480
75 Val Arg Lys Ala Lys Ala Lys Asn Leu Gln Lys Gln Arg Glu Arg Glu
76 145          150          155          160
78 tcc tgc tgg gct cag atc aac ttc acc aat aca gac atg tcc ttt gat 528
79 Ser Cys Trp Ala Gln Ile Asn Phe Thr Asn Thr Asp Met Ser Phe Asp
80          165          170          175
82 aac tct ctg ttt gct atc tcc acg aaa atg act cag gaa gac tca gtg 576
83 Asn Ser Leu Phe Ala Ile Ser Thr Lys Met Thr Gln Glu Asp Ser Val
84          180          185          190
86 gca acc cta gac tca ggg cct cgg aag agg ccc acc tct gca tca tcc 624
87 Ala Thr Leu Asp Ser Gly Pro Arg Lys Arg Pro Thr Ser Ala Ser Ser
88          195          200          205
90 tct ccg gag ccc cct gag ttc agc act ttc cgg gcc tgc cag tga 669
91 Ser Pro Glu Pro Pro Glu Phe Ser Thr Phe Arg Ala Cys Gln
92          210          215          220
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96 <211> LENGTH: 222
97 <212> TYPE: PRT
98 <213> ORGANISM: Mus musculus
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104 Ala Pro Ser Ile Ser Leu Val Pro Pro Tyr Pro Ser Ser His Glu Asp
105          20          25          30
107 Pro Ile Tyr Ile Ser Cys Thr Ala Pro Gly Asp Ile Leu Gly Ala Asn
108          35          40          45
110 Phe Thr Leu Phe Arg Gly Gly Glu Val Val Gln Leu Leu Gln Ala Pro
111          50          55          60
113 Ser Asp Arg Pro Asp Val Thr Phe Asn Val Thr Gly Gly Gly Ser Gly
114 65          70          75          80
116 Gly Gly Gly Glu Ala Ala Gly Gly Asn Phe Cys Cys Gln Tyr Gly Val
117          85          90          95
119 Met Gly Glu His Ser Gln Pro Gln Leu Ser Asp Phe Ser Gln Gln Val
120          100          105          110
122 Gln Val Ser Phe Pro Val Pro Thr Trp Ile Leu Ala Leu Ser Leu Ser
123          115          120          125
125 Leu Ala Gly Ala Val Leu Phe Ser Gly Leu Val Ala Ile Thr Val Leu
126          130          135          140
128 Val Arg Lys Ala Lys Ala Lys Asn Leu Gln Lys Gln Arg Glu Arg Glu

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Input Set : A:\082368-008600US.txt

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129 145          150          155          160
131 Ser Cys Trp Ala Gln Ile Asn Phe Thr Asn Thr Asp Met Ser Phe Asp
132          165          170          175
134 Asn Ser Leu Phe Ala Ile Ser Thr Lys Met Thr Gln Glu Asp Ser Val
135          180          185          190
137 Ala Thr Leu Asp Ser Gly Pro Arg Lys Arg Pro Thr Ser Ala Ser Ser
138          195          200          205
140 Ser Pro Glu Pro Pro Glu Phe Ser Thr Phe Arg Ala Cys Gln
141          210          215          220

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144 <210> SEQ ID NO: 3

145 <211> LENGTH: 579

146 <212> TYPE: DNA

147 <213> ORGANISM: Mus musculus

149 <220> FEATURE:

150 <221> NAME/KEY: CDS

151 <222> LOCATION: (1)..(579)

152 <223> OTHER INFORMATION:

W--> 154 <400> 3

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157 1          5          10          15
159 gca cca tcc atc tcc ttg gtg ccc ccc tac cca agc agc cac gag gac      96
160 Ala Pro Ser Ile Ser Leu Val Pro Pro Tyr Pro Ser Ser His Glu Asp
161          20          25          30
163 ccc atc tac atc tgc tgc aca gcc cca ggg gac atc cta ggg gcc aat      144
164 Pro Ile Tyr Ile Ser Cys Thr Ala Pro Gly Asp Ile Leu Gly Ala Asn
165          35          40          45
167 ttt acc ctg ttc cga ggg gga gag gtg gtc cag cta cta cag gcc ccc      192
168 Phe Thr Leu Phe Arg Gly Gly Glu Val Val Gln Leu Leu Gln Ala Pro
169          50          55          60
171 tca gat cgg cct gat gta aca ttc aat gtg act ggt ggt ggc agt ggt      240
172 Ser Asp Arg Pro Asp Val Thr Phe Asn Val Thr Gly Gly Gly Ser Gly
173 65          70          75          80
175 ggt ggc ggt gag gct gct ggg ggg aac ttc tgc tgt caa tat ggt gtg      288
176 Gly Gly Gly Glu Ala Ala Gly Gly Asn Phe Cys Cys Gln Tyr Gly Val
177          85          90          95
179 atg ggt gag cac agt cag ccc cag ctg tgc gac ttc agc cag cag gtg      336
180 Met Gly Glu His Ser Gln Pro Gln Leu Ser Asp Phe Ser Gln Gln Val
181          100          105          110
183 cag gtc tcc ttc cca gct aaa gcc aaa aac tta cag aag cag aga gag      384
184 Gln Val Ser Phe Pro Ala Lys Ala Lys Asn Leu Gln Lys Gln Arg Glu
185          115          120          125
187 cgt gaa tcc tgc tgg gct cag atc aac ttc acc aat aca gac atg tcc      432
188 Arg Glu Ser Cys Trp Ala Gln Ile Asn Phe Thr Asn Thr Asp Met Ser
189          130          135          140
191 ttt gat aac tct ctg ttt gct atc tcc acg aaa atg act cag gaa gac      480
192 Phe Asp Asn Ser Leu Phe Ala Ile Ser Thr Lys Met Thr Gln Glu Asp
193 145          150          155          160
195 tca gtg gca acc cta gac tca ggg cct cgg aag agg ccc acc tct gca      528

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196 Ser Val Ala Thr Leu Asp Ser Gly Pro Arg Lys Arg Pro Thr Ser Ala
197                               165                               170                               175
199 tca tcc tct ccg gag ccc cct gag ttc agc act ttc cgg gcc tgc cag      576
200 Ser Ser Ser Pro Glu Pro Pro Glu Phe Ser Thr Phe Arg Ala Cys Gln
201                               180                               185                               190
203 tga      579
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207 <211> LENGTH: 192
208 <212> TYPE: PRT
209 <213> ORGANISM: Mus musculus
211 <400> SEQUENCE: 4
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216                               20                               25                               30
218 Pro Ile Tyr Ile Ser Cys Thr Ala Pro Gly Asp Ile Leu Gly Ala Asn
219                               35                               40                               45
221 Phe Thr Leu Phe Arg Gly Gly Glu Val Val Gln Leu Leu Gln Ala Pro
222                               50                               55                               60
224 Ser Asp Arg Pro Asp Val Thr Phe Asn Val Thr Gly Gly Gly Ser Gly
225 65                               70                               75                               80
227 Gly Gly Gly Glu Ala Ala Gly Gly Asn Phe Cys Cys Gln Tyr Gly Val
228                               85                               90                               95
230 Met Gly Glu His Ser Gln Pro Gln Leu Ser Asp Phe Ser Gln Gln Val
231                               100                              105                              110
233 Gln Val Ser Phe Pro Ala Lys Ala Lys Asn Leu Gln Lys Gln Arg Glu
234                               115                              120                              125
236 Arg Glu Ser Cys Trp Ala Gln Ile Asn Phe Thr Asn Thr Asp Met Ser
237                               130                              135                              140
239 Phe Asp Asn Ser Leu Phe Ala Ile Ser Thr Lys Met Thr Gln Glu Asp
240 145                              150                              155                              160
242 Ser Val Ala Thr Leu Asp Ser Gly Pro Arg Lys Arg Pro Thr Ser Ala
243                               165                               170                               175
245 Ser Ser Ser Pro Glu Pro Pro Glu Phe Ser Thr Phe Arg Ala Cys Gln
246                               180                              185                              190
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250 <211> LENGTH: 690
251 <212> TYPE: DNA
252 <213> ORGANISM: Homo sapiens
254 <220> FEATURE:
255 <221> NAME/KEY: CDS
256 <222> LOCATION: (1)..(690)
257 <223> OTHER INFORMATION:
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262 1                               5                               10                               15
264 gca cca tcc atc cgg ctg gtg ccc ccg tac cca agc agc caa gag gac      96
265 Ala Pro Ser Ile Arg Leu Val Pro Pro Tyr Pro Ser Ser Gln Glu Asp

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TIME: 09:27:23

Input Set : A:\082368-008600US.txt

Output Set: N:\CRF4\08082006\J587841.raw

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266          20          25          30
268 ccc atc cac atc gca tgc atg gcc cct ggg aac ttc ccg ggg gcg aat      144
269 Pro Ile His Ile Ala Cys Met Ala Pro Gly Asn Phe Pro Gly Ala Asn
270          35          40          45
272 ttc aca ctg tat cga ggg ggg cag gtg gtc cag ctg ctg cag gcc ccc      192
273 Phe Thr Leu Tyr Arg Gly Gly Gln Val Val Gln Leu Leu Gln Ala Pro
274          50          55          60
276 acg gac cag cgc ggg gtg aca ttt aac ctg agc ggc ggc agc agc aag      240
277 Thr Asp Gln Arg Gly Val Thr Phe Asn Leu Ser Gly Gly Ser Ser Lys
278 65          70          75          80
280 gct cca ggg gga ccc ttc cac tgc cag tat gga gtg tta ggt gag ctg      288
281 Ala Pro Gly Gly Pro Phe His Cys Gln Tyr Gly Val Leu Gly Glu Leu
282          85          90          95
284 aac cag tcc cag ctg tca gac ctg agc gag ccc gtg aac gtc tcc ttc      336
285 Asn Gln Ser Gln Leu Ser Asp Leu Ser Glu Pro Val Asn Val Ser Phe
286          100          105          110
288 cca gtg ccc act tgg atc ttg gtg ctg tcc ctg agc ctg gct ggt gcc      384
289 Pro Val Pro Thr Trp Ile Leu Val Leu Ser Leu Ser Leu Ala Gly Ala
290          115          120          125
292 ctg ttc ctg ctt gct ggg ctg gtg gct gtt gcc ctg gtg gtc aga aaa      432
293 Leu Phe Leu Leu Ala Gly Leu Val Ala Val Ala Leu Val Val Arg Lys
294          130          135          140
296 gtt aaa ctg aga aat tta cag aag aaa aga gat cga gaa tcc tgc tgg      480
297 Val Lys Leu Arg Asn Leu Gln Lys Lys Arg Asp Arg Glu Ser Cys Trp
298 145          150          155          160
300 gcc cag att aac ttc gac agc aca gac atg tcc ttc gat aac tcc ctg      528
301 Ala Gln Ile Asn Phe Asp Ser Thr Asp Met Ser Phe Asp Asn Ser Leu
302          165          170          175
304 ttt acc gtc tcc gcg aaa acg atg cca gaa gaa gac ccg gcc acc ttg      576
305 Phe Thr Val Ser Ala Lys Thr Met Pro Glu Glu Asp Pro Ala Thr Leu
306          180          185          190
308 gat gat cac tca ggc acc act gcc acc ccc agc aac tcc agg acc cgg      624
309 Asp Asp His Ser Gly Thr Thr Ala Thr Pro Ser Asn Ser Arg Thr Arg
310          195          200          205
312 aag agg ccc act tcc acg tcc tcc tcg cct gag acc ccc gaa ttc agc      672
313 Lys Arg Pro Thr Ser Thr Ser Ser Ser Pro Glu Thr Pro Glu Phe Ser
314          210          215          220
316 act ttc cgg gcc tgc cag      690
317 Thr Phe Arg Ala Cys Gln
318 225          230
321 <210> SEQ ID NO: 6
322 <211> LENGTH: 230
323 <212> TYPE: PRT
324 <213> ORGANISM: Homo sapiens
326 <400> SEQUENCE: 6
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328 1          5          10          15
330 Ala Pro Ser Ile Arg Leu Val Pro Pro Tyr Pro Ser Ser Gln Glu Asp
331          20          25          30

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/587,841

DATE: 08/08/2006

TIME: 09:27:24

Input Set : A:\082368-008600US.txt

Output Set: N:\CRF4\08082006\J587841.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:37 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:35
L:154 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:152
L:259 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:257